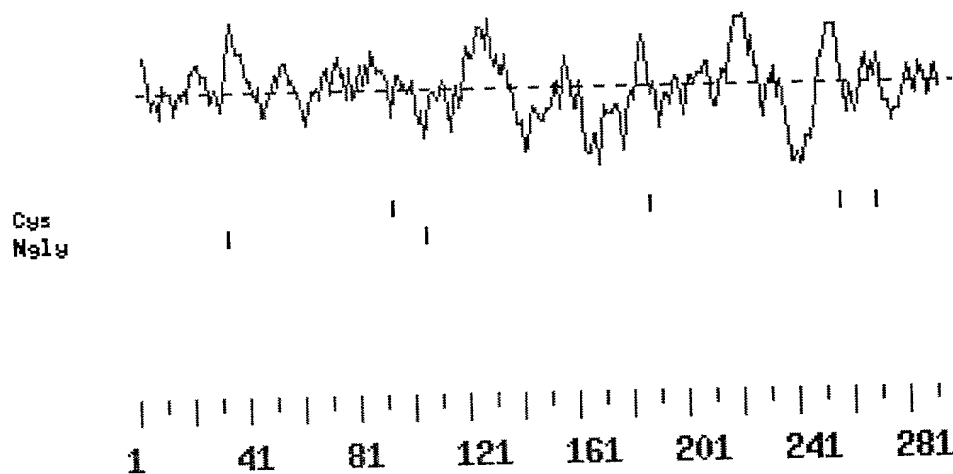


PFAM



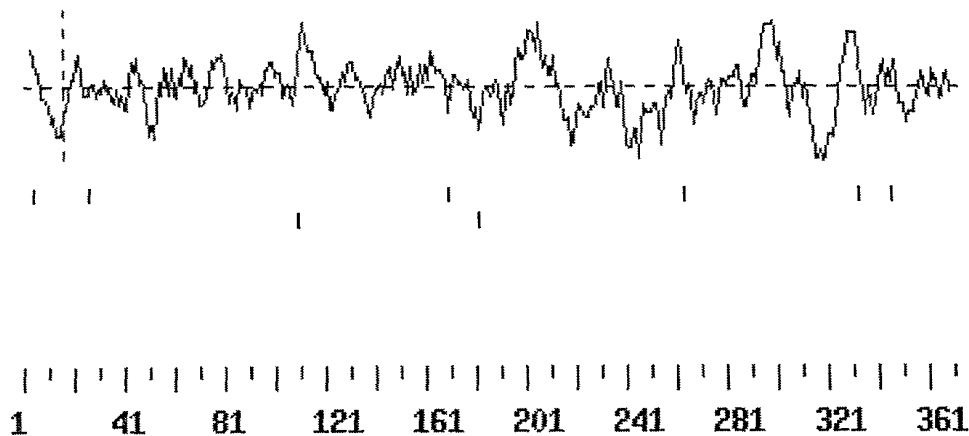
>8Apro

MLAAPINPSDINMIQGNYGLLPELPAVGGNEGVAQVVAVGSNVTGLKPGDWVIPANAGLG
TWRTEAVFSEEALIQVPSDIPLOSAATLGVPNCTAYRMLMDFEQLQPGDSVIQNASNSGV
GQAVIQIAAALGLRTINVVRDRPDIQKLSDRKSLGAEHVITEEELRRPEMKNFFKDMPQ
PRLALNCVGGKSSTELLRQLARGGTMVTYGGMAKQPVVASVSLIFKDLKLRGFWLSQWK
KDHSPDQFKELILTLCDLIRRGQLTAPACSQVPLQDYQSALEASMKPFISSKQILTM

FIGURE 1

PFAM

Cys
Ngly



>8Bpro

MWVCSTLWRVRTPARQWRGLLPASGCHGPAASSYSASAEPARVRALVYGHGDPKVVVEL
KNLELAAVRGSDVRVKMLAAPINPSDINMIQGNYGLLPELPAVGGNEGVAQVAVGNSVT
GLKPGDWVIPANAGLGTWRTEAVFSEEALIQVPSDIPLOSAATLGVPCTAYRMLMDFEQ
LQPGDSVIQNASNSGVGQAVIQIAAALGLRTINVVRDRPDIQKLSDRKSLGAEHVITEE
ELRRPEMKNEFFKDMPPRLALNCVGGKSSTELLRQLARGGTMVTYGGMAKQPVVASVSL
IFKDLKLRGFWSQWKKDHSPDQFKELILTLCDLIRRGQLTAPACSQVPLQDYQSALEAS
MKPFISSKQILTM

FIGURE 2

adh_zinc: domain 1 of 1, from 1 to 297: score 163.0, E = 5.2e-45
 *->pleveevvppepgpgeVlvkvkaaGiCgsDlhiykgglGlmypgpgd
 1 aa i++sD+ +++g y+
 8Apro 1 ML-----AAPINPSDINMIQGN---YGLL-- 21
 gthlfpvklPlvlGHEgaGvVeeVGsgVtgfklkvkgfkvGDrVvvlplv
 + lP v+G Eg+ +V++VGs+Vtg +k+GD V+++ +
 8Apro 22 -----PELPAVGGNEGVAQVAVGSNVTG-----LKP GDWVIPANAG 58
 gcCgrgsaeCefCkgsGrenlCpkgratgpgkGlm pndgfggftpkkgga
 8Apro 59 L----- 59
 PckGkdgyhfmgdGgfaEYvvvparrndyfvvkiPdgl ddeipleeaeaA
 G++ + +v ++ ++ +P ++ pl A
 8Apro 60 -----GTWRTEAVFSEE----ALIQVPSDI----PLQS---A 85
 allgcaglTaygalvraakvgs lppGdtVlVhGaGGGVGlaAvqlAkaaG
 a lg++ +Tay++l ++++ l+pGd+V + GVG+a++q+A a+G
 8Apro 86 ATLGVN PCTAYRMLMDFEQ---LQPGDSVIQNASNSGVGQAVIQIAAALG 132
 AarViavdssed.pekklelAkelGAdldadfvnnskglptvnddrkedf
 +++ +v ++d ++ + l+ +lG a++v+ ++e
 8Apro 133 LRTINVVRDPDiQKLS DRLK-SLG----AEHVIT-----EEELR 167
 veaikeltgGrngagGvDvvldcvGiglggatldaalallkpgGrlvvvG
 ++k +++ + + +l+c +gg++ ++l+ l++gG++v+ G
 8Apro 168 RPEMKNFFKDM---PQPR LALNC---VGGKSSTELLRQLARGGTMV TYG 210
 pkvavGvpvgggapipl..lllkeeklyersikGsflggrkprlsvlsvd
 G++ ++ +++ l++k ++++G++l+++k +
 8Apro 211 -----GMAKQPVVASVs lLIFKD-----LKL RGFWLSQWKKD----- 242
 ttpdelreal dllasgikdkngkgvldplithtlpplddsleeaneAfel
 ++pd ++e++ l ++i+ +g+l ++p l + + A+e+
 8Apro 243 HSPDQFKELILTLC DLIR----RGQLTAPACSQVP-LQ----DYQSALEA 283
 lesghk.gkvvlip<-*
 ++ ++ k++l++
 8Apro 284 SMKPFIsSKQILTM 297

FIGURE 3

adh_zinc: domain 1 of 1, from 57 to 373: score 212.3, E = 7.4e-60

```

      *->pleveevpvpepgpgeVlvkvkaaGiCgsDlhiykgglGlmypgpgd
            ++e++  +++  +  +V+vk+aa i++sD+  +++g      y+
8Bpro    57      VVELKNLELAAVRGSDVRVKMLAAPINPSDINMIQGN----YGLL-- 97

            gthlfpvklPlvlGHEgaGvVeeVGsgVtgfklkvvgkfkvGDrVvvlplv
            + 1P v+G Eg+ +V++VGs+Vtg      +k+GD V+++  +
8Bpro    98 -----PELPAVGGNEGVAQVVAVGSNVTG-----LKPGDWVIPANAG 134

            gcCgrgsaeCefCkgsGrenlCpkgratgpgkGlmrndgfggftpkkqga

8Bpro    135 L----- 135

            PckGkdgyhfmgdGgfaEYvvvparrndyfvvkiPdgldeipleeaeaA
            G++ + +v ++      ++ +P ++      pl      A
8Bpro    136 -----GTWRTEAVFSEE-----ALIQVPSDI-----PLQS---A 161

            allgcaglTaygalvraakvgslppGdtVlVhGaGGGVGlaAvqlAkaaG
            a lg++ +Tay++l +++++  l+pGd+V      +  GVG+a++q+A a+G

8Bpro    162 ATLGVPNCTAYRMLMDFEQ---LQPGDSVIQNASNSGVGQAVIQIAAALG 208

            AarViavdssed.pekklelAkelGAdldadfvnnskglptvnddrkedf
            +++ +v  ++d ++  + l+ +lG      a++v+      ++e
8Bpro    209 LRTINVVRDRPDiQKLSDRLK-SLG---AEHVIT-----EEELR 243

            veaikeltgGrngagGvDvldcvGiglggatldaalallkpgGrlvvvG
            ++k +++      + +  +l+c      +gg++  ++l+ l++gG++v+ G
8Bpro    244 RPEMKNFFKDM---PQPRALALNC---VGGKSSTELLRQLARGGTMVTYG 286

            pkvavGvpgggapipl..lllkeeeeklyersikGsflggrkprlsvlsvd
            G++  ++ +++ l++k      ++++G++l+++k +
8Bpro    287 -----GMAKQPVASVsllLIFKD-----LKLRFWLSQWKKD----- 318

            ttpdelrealdllasgikdkngkgvldplithtlpplddsleeaneAfel
            ++pd ++e++  l ++i+      +g+l      ++p l      + + A+e+
8Bpro    319 HSPDQFKELILTLCDLIR---RGQLTAPACSQVP-LQ---DYQSALEA 359

            lesgh.kkvvlip<-*
            ++  ++ k++l++
8Bpro    360 SMKPFIsSKQILTM      373

```

FIGURE 4